ATGTTCGGCTCCGCCCCCCAGCGTCCCGTGGCCATGACGACCGCTCAGAGGGACTCCCTG

TTGTGGAAGCTCGCGGGGGTTGCTGCGGGAGTCCGGGGATGTGGTCCTGTCTGGCTGTAGC

ACCCTGAGCCTGCTGACTCCCACACTGCAACAGCTGAACCACGTATTTGAGCTGCACCTG

GGGCCATGGGGCCCTGGCCAGACAGGCTTTGTGGCTCTGCCCTCCCATCCTGCCGACTCC

CCTGTTATTCTTCAGCTTCAGTTTCTCTTCGATGTGCTGCAGAAAACACTTTCACTCAAG

CTGGTCCATGTTGCTGGTCCTGGCCCCACAGGGCCCATCAAGATTTTCCCCTTCAAATCC

CTTCGGCACCTGGAGCTCCGAGGTGTTCCCCTCCACTGTCTGCATGGCCTCCGAGGCATC

TACTCCCAGCTGGAGACCCTGATTTGCAGCAGGAGCCTCCAGGCATTAGAGGAGCTCCTC

TCAGCCTGCGGCGGCGACTTCTGCTCTGCCCTCCCTTGGCTGGCTCTGCTTTCTGCCAAC

TTCAGCTACAATGCACTGACCGCCTTAGACAGCTCCCTGCGCCTCTTGTCAGCTCTGCGT

TTCTTGAACCTAAGCCACAATCAAGTCCAGGACTGTCAGGGATTCCTGATGGATTTGTGT

GAGCTCCACCATCTGGACATCTCCTATAATCGCCTGCATTTGGTGCCAAGAATGGGACCC

TCAGGGGCTGCTCTGGGGGTCCTGATACTGCGAGGCAATGAGCTTCGGAGCCTGCATGGC

CTAGAGCAGCTGAGGAATCTGCGGCACCTGGATTTGGCATACAACCTGCTGGAAGGACAC

CGGGAGCTGTCACCACTGTGGCTGCTGGCTGAGCTCCGCAAGCTCTACCTGGAGGGGAAC

CCTCTTTGGTTCCACCCTGAGCACCGAGCAGCCACTGCCCAGTACTTGTCACCCCGGGCC

AGGGATGCTGCTACTGGCTTCCTTCTCGATGGCAAGGTCTTGTCACTGACAGATTTTCAG

ACTCACACATCCTTGGGGCTCAGCCCCATGGGCCCACCTTTGCCCTGGCCAGTGGGGAGT

ACTCCTGAAACCTCAGGTGGCCCTGACCTGAGTGACAGCCTCTCCTCAGGGGGTGTTGTG

ACCCAGCCCCTGCTTCATAAGGTTAAGAGCCGAGTCCGTGTGAGGCGGGCAAGCATCTCT

GAACCCAGTGATACGGACCCGGAGCCCCGAACTCTGAACCCCTCTCCGGCTGGATGGTTC

GTGCAGCAGCACCCGGAGCTGGAGCTCATGAGCAGCTTCCGGGAACGGTTCGGCCGCAAC

TGGCTGCAGTACAGGAGTCACCTGGAGCCCTCCGGAAACCCTCTGCCGGCCACCCCCACT

Figure 1A

ACTTCTGCACCCAGTGCACCTCCAGCCAGCTCCCAGGGCCCCGACACTGCACCCAGACCT

TCACCCCCGCAGGAGGAAGCCAGAGGCCCCCAGGAGTCACCACAGAAAATGTCAGAGGAG

GTCAGGGCGGAGCCACAGGAGGAGGAAGAGGAGAAGGAGGGGAAGGAGGAGAAGGAGGAG

GGGGAGATGGTGGAACAGGGAGAAGAGGAGGCAGGAGAGGAGGAAGAAGAGGAGCAGGAC

CAGAAGGAAGTGGAAGCGGAACTCTGTCGCCCCTTGTTGGTGTGTCCCCTGGAGGGGCCT

GAGGGCATACGGGGCAGGGAATGCTTTCTCAGGGTCACTTCTGCCCACCTGTTTGAGGTG

GAACTCCAAGCAGCTCGCACCTTGGAGCGACTGGAGCTCCAGAGTCTGGAGGCAGCTGAG

ATAGAGCCGGAGGCCCAGGCCCAGAGGTCGCCCAGGCCCACGGGCTCAGATCTGCTCCCT

GGAGCCCCCATCCTCAGTCTGCGCTTCTCCTACATCTGCCCTGACCGGCAGTTGCGTCGC

TATTTGGTGCTGGAGCCTGATGCCCACGCAGCTGTCCAGGAGCTGCTTGCCGTGTTGACC

CCAGTCACCAATGTGGCTCGGGAACAGCTTGGGGAGGCCAGGGACCTCCTGCTGGGTAGA

TTCCAGTGTCTACGCTGTGGCCATGAGTTCAAGCCAGAGGAGCCCAGGATGGGATTAGAC

AGTGAGGAAGGCTGGAGGCCTCTGTTCCAAAAGACAGGGAGCGGAAACAGGGAGAGCAGT

CTCTGGCTCCTTCTCCGTTTGCCAGCCCTGTCTGCCACCCTCCTGGCCATGGTGACCACC

TTGACAGGGCCAAGAACAGCCCACCTCAGGCACCGAGCACCCGTGACCATGGTAGTTGGA

GCCTCAGTCCCCCCCCTGAGCGCTGTGGCCTCCGCTCTGTGGACCACCGACTCCGGCTCT

TCCTGGATGTTGAGGTGTTCAGCGATGCCCAGGAGGAGTTCCAGTGCTGCCTCAAGGTGC

CAGTGGCATTGGCAGGCCACACTGGGGAGTTCATGTGCCTTGTGGTTGTGTCTGACCGCA

GGCTGTACCTGTTGA

Figure 1B.

ATGTTCGGCTCCGCCCCCCAGCGTCCCGTGGCCATGACGACCGCTCAGAGGGACTCCCTG

TTGTGGAAGCTCGCGGGGGTTGCTGCGGGAGTCCGGGGATGTGGTCCTGTCTGGCTGTAGC

ACCCTGAGCCTGCTGACTCCCACACTGCAACAGCTGAACCACGTATTTGAGCTGCACCTG

5   GGGCCATGGGGCCCTGGCCAGACAGGCTTTGTGGCTCTGCCCTCCCATCCTGCCGACTCC

CCTGTTATTCTTCAGCTTCAGTTTCTCTTCGATGTGCTGCAGAAAACACTTTCACTCAAG

CTGGTCCATGTTGCTGGTCCTGGCCCCACAGGGCCCATCAAGATTTTCCCCTTCAAATCC

CTTCGGCACCTGGAGCTCCGAGGTGTTCCCCTCCACTGTCTGCATGGCCTCCGAGGCATC

TACTCCCAGCTGGAGACCCTGATTTGCAGCAGGAGCCTCCAGGCATTAGAGGAGCTCCTC

10   TCAGCCTGCGGCGGCGACTTCTGCTCTGCCCTCCCTTGGCTGGCTCTGCTTTCTGCCAAC

TTCAGCTACAATGCACTGACCGCCTTAGACAGCTCCCTGCGCCTCTTGTCAGCTCTGCGT

TTCTTGAACCTAAGCCACAATCAAGTCCAGGACTGTCAGGGATTCCTGATGGATTTGTGT

GAGCTCCACCATCTGGACATCTCCTATAATCGCCTGCATTTGGTGCCAAGAATGGGACCC

TCAGGGGCTGCTCTGGGGGTCCTGATACTGCGAGGCAATGAGCTTCGGAGCCTGCATGGC

15   CTAGAGCAGCTGAGGAATCTGCGGCACCTGGATTTGGCATACAACCTGCTGGAAGGACAC

CGGGAGCTGTCACCACTGTGGCTGCTGGCTGAGCTCCGCAAGCTCTACCTGGAGGGGAAC

CCTCTTTGGTTCCACCCTGAGCACCGAGCAGCCACTGCCCAGTACTTGTCACCCCGGGCC

AGGGATGCTGCTACTGGCTTCCTTCTCGATGGCAAGGTCTTGTCACTGACAGATTTTCAG

ACTCACACATCCTTGGGGCTCAGCCCCATGGGCCCACCTTTGCCCTGGCCAGTGGGGAGT

20   ACTCCTGAAACCTCAGGTGGCCCTGACCTGAGTGACAGCCTCTCCTCAGGGGGTGTTGTG

ACCCAGCCCCTGCTTCATAAGGTTAAGAGCCGAGTCCGTGTGAGGCGGGCAAGCATCTCT

GAACCCAGTGATACGGACCCGGAGCCCCGAACTCTGAACCCCTCTCCGGCTGGATGGTTC

GTGCAGCAGCACCCGGAGCTGGAGCTCATGAGCAGCTTCCGGGAACGGTTCGGCCGCAAC

25   **Figure 2A**

3053-4093US1

TGGCTGCAGTACAGGAGTCACCTGGAGCCCTCCGGAAACCCTCTGCCGGCCACCCCCACT

ACTTCTGCACCCAGTGCACCTCCAGCCAGCTCCCAGGGCCCCGACACTGCACCCAGACCT

TCACCCCCGCAGGAGGAAGCCAGAGGCCCCCAGGAGTCACCACAGAAAATGTCAGAGGAG

5   GTCAGGGCGGAGCCACAGGAGGAGGAAGAGGAGAAGGAGGGGAAGGAGGAGAAGGAGGAG

GGGGAGATGGTGGAACAGGGAGAAGAGGAGGCAGGAGAGGAGGAAGAAGAGGAGCAGGAC

CAGAAGGAAGTGGAAGCGGAACTCTGTCGCCCCTTGTTGGTGTGTCCCCTGGAGGGGCCT

GAGGGCGTACGGGGCAGGGAATGCTTTCTCAGGGTCACTTCTGCCCACCTGTTTGAGGTG

GAACTCCAAGCAGCTCGCACCTTGGAGCGACTGGAGCTCCAGAGTCTGGAGGCAGCTGAG

10   ATAGAGCCGGAGGCCCAGGCCCAGAGGTCGCCCAGGCCCACGGGCTCAGATCTGCTCCCT

GGAGCCCCCATCCTCAGTCTGCGCTTCTCCTACATCTGCCCTGACCGGCAGTTGCGTCGC

TATTTGGTGCTGGAGCCTGATGCCCACGCAGCTGTCCAGGAGCTGCTTGCCGTGTTGACC

CCAGTCACCAATGTGGCTCGGGAACAGCTTGGGGAGGCCAGGGACCTCCTGCTGGGTAGA

TTCCAGTGTCTACGCTGTGGCCATGAGTTCAAGCCAGAGGAGCCCAGGATGGGATTAGAC

15   AGTGAGGAAGGCTGGAGGCCTCTGTTCCAAAAGACAGAATCTCCTGCTGTGTGTCCTAAC

TGTGGTAGTGACCACGTGGTTCTCCTCGCTGTGTCTCGGGGAACCCCCAACAGGGAGCGG

AAACAGGGAGAGCAGTCTCTGGCTCCTTCTCCGTTTGCCAGCCCTGTCTGCCACCCTCCT

GGCCATGGTGACCACCTTGACAGGGCCAAGAACAGCCCACCTCAGGCACCGAGCACCCGT

GACCATGGTAGTTGGAGCCTCAGTCCCCCCCCTGAGCGCTGTGGCCTCCGCTCTGTGGAC

20   CACCGACTCCGGCTCTTCCTGGATGTTGAGGTGTTCAGCGATGCCCAGGAGGAGTTCCAG

TGCTGCCTCAAGGTGCCAGTGGCATTGGCAGGCCACACTGGGGAGTTCATGTGCCTTGTG

GTTGTGTCTGACCGCAGGCTGTACCTGTTGAAGGTGACTGGGGAGATGCGTGAGCCTCCA

GCTAGCTGGCTGCAGCTGACCCTGGCTGTTCCCCTGCAGGATCTGAGTGGCATAGAGCTG

25   **Figure 2B**

GGCCTGGCAGGCCAGAGCCTGCGGCTAGAGTGGGCAGCTGGGGCGGGCCGCTGTGTGCTG

CTGCCCCGAGATGCCAGGCATTGCCGGGCCTTCCTAGAGGAGCTCCTTGATGTCTTGCAG

TCTCTGCCCCCTGCCTGGAGGAACTGTGTCAGTGCCACAGAGGAGGAGGTCACCCCCCAG

5   CACCGGCTCTGGCCATTGCTGGAAAAAGACTCATCCTTGGAGGCTCGCCAGTTCTTCTAC

CTTCGGGCGTTCCTGGTTGAAGGCCCTTCCACCTGCCTCGTATCCCTGTTGCTGACTCCG

TCCACCCTGTTCCTGTTAGATGAGGATGCTGCAGGGTCCCCGGCAGAGCCCTCTCCTCCA

GCAGCATCTGGCGAAGCCTCTGAGAAGGTGCCTCCCTCGGGGCCGGGCCCTGCTGTGCGT

GTCAGGGAGCAGCAGCCACTCAGCAGCCTGAGCTCCGTGCTGCTCTACCGCTCAGCCCCT

GAGGACTTGCGGCTGCTCTTCTACGATGAGGTGTCCCGGCTGGAGAGCTTTTGGGCACTC

CGTGTGGTGTGTCAGGAGCAGCTGACAGCCCTGCTTGCCTGGATCCGGGAACCATGGGAG

GAGCTGTTTTCCATCGGACTCCGGACAGTGATCCAAGAGGCGCTGGCCCTTGACCGATGA

Figure 2C.

MFGSAPQRPVAMTTAQRDSLLWKLAGLLRESGDVVLSGCSTLSLLTPTLQQLNHVFELHL

GPWGPGQTGFVALPSHPADSPVILQLQFLFDVLQKTLSLKLVHVAGPGPTGPIKIFPFKS

LRHLELRGVPLHCLHGLRGIYSQLETLICSRSLQALEELLSACGGDFCSALPWLALLSAN

FSYNALTALDSSLRLLSALRFLNLSHNQVQDCQGFLMDLCELHHLDISYNRLHLVPRMGP

5   SGAALGVLILRGNELRSLHGLEQLRNLRHLDLAYNLLEGHRELSPLWLLAELRKLYLEGN

PLWFHPEHRAATAQYLSPRARDAATGFLLDGKVLSLTDFQTHTSLGLSPMGPPLPWPVGS

TPETSGGPDLSDSLSSGGVVTQPLLHKVKSRVRVRRASISEPSDTDPEPRTLNPSPAGWF

VQQHPELELMSSFRERFGRNWLQYRSHLEPSGNPLPATPTTSAPSAPPASSQGPDTAPRP

SPPQEEARGPQESPQKMSEEVRAEPQEEEEEKEGKEEKEEGEMVEQGEEEAGEEEEEEQD

10   QKEVEAELCRPLLVCPLEGPEGIRGRECFLRVTSAHLFEVELQAARTLERLELQSLEAAE

IEPEAQAQRSPRPTGSDLLPGAPILSLRFSYICPDRQLRRYLVLEPDAHAAVQELLAVLT

PVTNVAREQLGEARDLLLGRFQCLRCGHEFKPEEPRMGLDSEEGWRPLFQKTGSGNRESS

LWLLLRLPALSATLLAMVTTLTGPRTAHLRHRAPVTMVVGASVPPLSAVASALWTTDSGS

SWMLRCSAMPRRSSSAASRCQWHWQATLGSSCALWLCLTAGCTC

15

Figure 3.

3053-4093US1

MFGSAPQRPVAMTTAQRDSLLWKLAGLLRESGDVVLSGCSTLSLLTPTLQQLNHVFELHL

GPWGPGQTGFVALPSHPADSPVILQLQFLFDVLQKTLSLKLVHVAGPGPTGPIKIFPFKS

LRHLELRGVPLHCLHGLRGIYSQLETLICSRSLQALEELLSACGGDFCSALPWLALLSAN

FSYNALTALDSSLRLLSALRFLNLSHNQVQDCQGFLMDLCELHHLDISYNRLHLVPRMGP

SGAALGVLILRGNELRSLHGLEQLRNLRHLDLAYNLLEGHRELSPLWLLAELRKLYLEGN

PLWFHPEHRAATAQYLSPRARDAATGFLLDGKVLSLTDFQTHTSLGLSPMGPPLPWPVGS

TPETSGGPDLSDSLSSGGVVTQPLLHKVKSRVRVRRASISEPSDTDPEPRTLNPSPAGWF

VQQHPELELMSSFRERFGRNWLQYRSHLEPSGNPLPATPTTSAPSAPPASSQGPDTAPRP

SPPQEEARGPQESPQKMSEEVRAEPQEEEEEKEGKEEKEEGEMVEQGEEEAGEEEEEEQD

QKEVEAELCRPLLVCPLEGPEGVRGRECFLRVTSAHLFEVELQAARTLERLELQSLEAAE

IEPEAQAQRSPRPTGSDLLPGAPILSLRFSYICPDRQLRRYLVLEPDAHAAVQELLAVLT

PVTNVAREQLGEARDLLLGRFQCLRCGHEFKPEEPRMGLDSEEGWRPLFQKTESPAVCPN

CGSDHVVLLAVSRGTPNRERKQGEQSLAPSPFASPVCHPPGHGDHLDRAKNSPPQAPSTR

DHGSWSLSPPPERCGLRSVDHRLRLFLDVEVFSDAQEEFQCCLKVPVALAGHTGEFMCLV

VVSDRRLYLLKVTGEMREPPASWLQLTLAVPLQDLSGIELGLAGQSLRLEWAAGAGRCVL

LPRDARHCRAFLEELLDVLQSLPPAWRNCVSATEEEVTPQHRLWPLLEKDSSLEARQFFY

LRAFLVEGPSTCLVSLLLTPSTLFLLDEDAAGSPAEPSPPAASGEASEKVPPSGPGPAVR

VREQQPLSSLSSVLLYRSAPEDLRLLFYDEVSRLESFWALRVVCQEQLTALLAWIREPWE

ELFSIGLRTVIQEALALDR

Figure 4.

```
>gi|6005788 imidazoline receptor candidate >gi|3462807|gb|AAC33104.1|
        (AF082516) I-1 receptor candidate protein [Homo sapiens]
        Length = 1504

 Score = 68.3 bits (164), Expect = 4e-10
 Identities = 69/256 (26%), Positives = 102/256 (38%), Gaps = 26/256 (10%)

Query: 107 VLQKTLSLKLVHVAGP-GPTG---------PIKIFPFKSLRHLELRGVPLHCLHGLRGIY 156
            +L  T  LK + V+G  GP G        P +  FKSL  +E+      + GL
Sbjct: 180 ILDFTCRLKYLKVSGTEGPFGTSNIQEQLLPFDLSIFKSLHQVEISHCDAKHIRGLVASK 239


Query: 157 SQLETLICSRSLQALEELL--------------SACGGDFCSALP-WLALLSANFSYNXX 201
             L TL   S  +++E+L                +   G   + +P W AL + + S+N
Sbjct: 240 PTLATLSVRFSATSMKEVLVPEASEFDEWEPEGTTLEGPVTAVIPTWQALTTLDLSHNSI 299


Query: 202 XXXXXXXXXXXXXXXXXXXXXHNQVQDCQGFLMDLCELHHLDISYNRLHLVPRMGPSGAALG 261
                                 HN +     L  L  L HLD+SYN+L  +  +          +
Sbjct: 300 SEIDESVKLIPKIEFLDLSHNGLLVVDN-LQHLYNLVHLDLSYNKLSSLEGLHTKLGNIK 358


Query: 262 VLILRGNELRSLHGLEQLRNLRHLDLAYNLLEGHRELSPLWLLAELRKLYLEGNPLWFHP 321
             L L GN L SL GL +L +L +LDL  N +E   E+  +  L L  + L  NPL   P
Sbjct: 359 TLNLAGNLLESLSGLHKLYSLVNLDLRDNRIEQMEEVRSIGSLPCLEHVSLLNNPLSIIP 418


Query: 322 EHRAATAQYLSPRARD 337
            ++R         RA +
Sbjct: 419 DYRTKVLAQFGERASE 434
```

Figure 5.

3053-4093US1

```
 101 TACGCTGTGGCCATGAGTTCAAGCCAGAGGAGCCCAGGATGGGATTAGAC 2150
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1644 TACGCTGTGGCCATGAGTTCAAGCCAGAGGAGCCCAGGATGGGATTAGAC 1693

2151 AGTGAGGAAGGCTGGAGGCCTCTGTTCCAAAAG................. 2183
     |||||||||||||||||||||||||||||||||
1694 AGTGAGGAAGGCTGGAGGCCTCTGTTCCAAAAGACAGAATCTCCTGCTGT 1743
                                            .

                                            .

                                            .

2184 .........ACAGGGAGCGGAAACAGGGAGAGCAGTCTCTGGCTCCTTCT 2224
              ||||||||||||||||||||||||||||||||||||||||||
1794 GAACCCCCAACAGGGAGCGGAAACAGGGAGAGCAGTCTCTGGCTCCTTCT 1843

2225 CCGTTTGCCAGCCCTGTCTGCCACCCTCCTGGCCATGGTGACCACCTTGA 2274
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1844 CCGTTTGCCAGCCCTGTCTGCCACCCTCCTGGCCATGGTGACCACCTTGA 1893




2825 TCATCCTTGGAGGCTCGCCAGTTCTTCTACCTTCGGGCGTTCCTGGTTGA 2874
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2444 TCATCCTTGGAGGCTCGCCAGTTCTTCTACCTTCGGGCGTTCCTGGTTGA 2493
                                            .

                                            .

                                            .

3375 ATCTGGGCCCCTCCATGACCTTCCACACTGGATGCCTCTTTCCCTGCAGG 3424
                                                     |||
2494 ...........................................AGG 2496

3425 CCCTTCCACCTGCCTCGTATCCCTGTTGCTGACTCCGTCCACCCTGTTCC 3474
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2497 CCCTTCCACCTGCCTCGTATCCCTGTTGCTGACTCCGTCCACCCTGTTCC 2546
```

Figure 6.

644655 v1

3053-4093US1

```
Query= sequence
         (1114 letters)

Database: newnr
          228,478 sequences; 162,186,938 total letters

Searching.................................................done

                                                         Score      E
Sequences producing significant alignments:              (bits)   Value

gb|AAF52305.1| (AE003611) CG9044 gene product [Drosophila melano...   127   5e-28
gi|6005788 imidazoline receptor candidate >gi|3462807|gb|AAC3310...    68   4e-10
gb|AAF57514.1| (AE003794) CG8595 gene product [Drosophila melano...    47   0.001


>gb|AAF52305.1| (AE003611) CG9044 gene product [Drosophila melanogaster]
         Length = 1289

 Score = 127 bits (317), Expect = 5e-28
 Identities = 99/321 (30%), Positives = 149/321 (45%), Gaps = 11/321 (3%)

Query: 38   KLAGLLRESGDVVXXXXXXXXXXXXXXXXXXXNHVF------ELHLGPWGPGQTGFVALPSH 91
            +LA LLR++GD +                   N F      E+ G        F +
Sbjct: 8    ELANLLRQNGDKILSSEFTLTLSGSLLRALNDSFTLIADTEIGTGAGYLQPQSFQVVKPI 67

Query: 92   PADSPVILQLQFLFDVLQKTLSLKLVHVAGPGP-TGPIKIFPFKSLRHLELRGVPLHCLH 150
              A S V   LQ + D +QKT LKL +        G I I F++LR LE+ + + +
Sbjct: 68   NAKSSVFPDLQLVHDFVQKTTLLKLTYFPSEHYFEGAIDIAKFRALRRLEVNKINIGQVV 127

Query: 151  GLRGIYSQLETLICSRSLQALEEELLSACGGDFCSALPWLALLSANFSYNXXXXXXXXXXX 210
            G++ +  QL+ LIC +SL ++++++ CGGD +   W L +A+FSYN
Sbjct: 128  GIQPLRGQLQHLICVKSLTSVDDIITRCGGDNSNGFVWNELKTADFSYNSLRSVDTALEF 187

Query: 211  XXXXXXXXXXHNQVQDCQGFLMDLCELHHLDISYNRLHLVPRMGPSGA-ALGVLILRGNE 269
                      HN++         + L  LD+SYN L  +P+         L +L + N
Sbjct: 188  AQHLQHLNLRHNKLTSVAA-IKWLPHLKTLDLSYNCLTHLPQFHMEACKRLQLLNISNNY 246

Query: 270  LRSLHGLEQLRNLRHLDLAYNLLEGHRELSPLWLLAELRKLYLEGNPLWFHPEHRAATAQ 329
            + L + +L L +LDL+ N L H +L PL L L  L+GNPL +P+HR ATAQ
Sbjct: 247  VEELLDVAKLDALYNLDLSDNCLLEHSQLLPLSALMSLIVLNLQGNPLACNPKHRQATAQ 306

Query: 330  YLSPRARDAATGFLLDGKVLS 350
            YL      A  F+LD + L+
Sbjct: 307  YL--HKNSATVKFVLDFEPLT 325
```

Figure 7A

644655 v1

```
Score = 41.4 bits (95), Expect = 0.054
Identities = 41/151 (27%), Positives = 62/151 (40%), Gaps = 20/151 (13%)

Query: 814  VDHRLRLFLDVEVFSDAQEEFQCCLKVPVALAGHTGEFMCLVVVSDRRLYLLKVTGEMRE 873
            +DHRL+L+     F +  E F+   K +              LVV+S+ + YL++   E +
Sbjct: 1018 IDHRLKLYFYQRKFKEDGEHFKWLAKGRIYNEQTQSLGEGLVVMSNCKCYLMEAFAEPHD 1077

Query: 874  PPASWLQLTLAVPLQDLSGIELGLAGQSLRLEWAAGA-------GRCVLLPRDARHCRAF 926
             A WL+  ++V +  L  I+L        L W G        G VLL   D
Sbjct: 1078 DVAKWLRQVVSVAVNRLVAIDL--------LPWKLGLSFTLKDWGGFVLLLHDMLR---- 1125

Query: 927  LEELLDVLQSLPPAWRNCVSATEEEVTPQHR 957
            E LL+ LQ +P    C   + VT H+
Sbjct: 1126 TESLLNYLQQIPLP-EQCKLNHQPSVTLSHQ 1155


>gi|6005788 imidazoline receptor candidate >gi|3462807|gb|AAC33104.1|
        (AF082516) I-1 receptor candidate protein [Homo sapiens]
        Length = 1504

 Score = 68.3 bits (164), Expect = 4e-10
 Identities = 69/256 (26%), Positives = 102/256 (38%), Gaps = 26/256 (10%)

Query: 107  VLQKTLSLKLVHVAGP-GPTG---------PIKIFPFKSLRHLELRGVPLHCLHGLRGIY 156
            +L  T  LK + +G  GP G         P +  FKSL  +E+     + GL
Sbjct: 180  ILDFTCRLKYLKVSGTEGPFGTSNIQEQLLPFDLSIFKSLHQVEISHCDAKHIRGLVASK 239

Query: 157  SQLETLICSRSLQALEELL--------------SACGGDFCSALP-WLALLSANFSYNXX 201
            L TL   S  +++E+L              +   G   + +P W AL + + S+N
Sbjct: 240  PTLATLSVRFSATSMKEVLVPEASEFDEWEPEGTTLEGPVTAVIPTWQALTTLDLSHNSI 299

Query: 202  XXXXXXXXXXXXXXXXXXXHNQVQDCQGFLMDLCELHHLDISYNRLHLVPRMGPSGAALG 261
                               HN +      L  L  L HLD+SYN+L  +   +       +
Sbjct: 300  SEIDESVKLIPKIEFLDLSHNGLLVVDN-LQHLYNLVHLDLSYNKLSSLEGLHTKLGNIK 358

Query: 262  VLILRGNELRSLHGLEQLRNLRHLDLAYNLLEGHRELSPLWLLAELRKLYLEGNPLWFHP 321
            L L GN L SL GL +L +L +LDL  N +E  E+ +   L L  + L NPL   P
Sbjct: 359  TLNLAGNLLESLSGLHKLYSLVNLDLRDNRIEQMEEVRSIGSLPCLEHVSLLNNPLSIIP 418

Query: 322  EHRAATAQYLSPRARD 337
            ++R        RA +
Sbjct: 419  DYRTKVLAQFGERASE 434
```

Figure 7B

```
FL1-18_SPLICE_VARIANT              ---MFGSAPQRPVAMTTAQRDS---LLWKLAGLLRESGD----------
FL1-18                            ---MFGSAPQRPVAMTTAQRDS---LLWKLAGLLRESGD----------
Drosophila_melanogaster_CG9044    ------MDPQK--------------ITELANLLRQNGD----------
imidazoline_receptor_candidate    MATARTFGPEREAEPAKEARVVGSELVDTYTVYIIQVTDGSHEWTVKHRY
                                        *::           .       :    :  : :    *

FL1-18_SPLICE_VARIANT             ---------VVLSGCSTLSLLTP--------------------------
FL1-18                            ---------VVLSGCSTLSLLTP--------------------------
Drosophila_melanogaster_CG9044    ---------KILSSEFTLTLSGS--------------------------
imidazoline_receptor_candidate    SDFHDLHEKLVAERKIDKNLLPPKKIIGKNSRSLVEKREKDLEVYLQKLL
                                             :  .        .*   .

FL1-18_SPLICE_VARIANT             ------TLQQLNHVFELHLG---------------------------PWG
FL1-18                            ------TLQQLNHVFELHLG---------------------------PWG
Drosophila_melanogaster_CG9044    ------LLRALNDSFTLIADT--------------------------EIG
imidazoline_receptor_candidate    AAFPGVTPRVLAHFLHFHFYEINGITAALAEELFEKGEQLLGAGEVFAIG
                                        : *  . : :                                *

FL1-18_SPLICE_VARIANT             PG----Q-TGFVALPSHPADSPVILQLQFLFDVLQKTLSLKLVHVAGPGP
FL1-18                            PG----Q-TGFVALPSHPADSPVILQLQFLFDVLQKTLSLKLVHVAGPGP
Drosophila_melanogaster_CG9044    TGAGYLQPQSFQVVKPINAKSSVFPDLQLVHDFVQKTTLLKLTYFPSEHY
imidazoline_receptor_candidate    PLQLYAVTEQLQQGKPTCASGDAKTDLGHILDFTCRLKYLKVSGTEGPFG
                                    .              :   *... :*  : *.  : **:

FL1-18_SPLICE_VARIANT             -------TGPIKIFPFKSLRHLELRGVPLHCLHGLRGIYSQLETLICSRS
FL1-18                            -------TGPIKIFPFKSLRHLELRGVPLHCLHGLRGIYSQLETLICSRS
Drosophila_melanogaster_CG9044    F------EGAIDIAKFRALRRLEVNKINIGQVVGIQPLRGQLQHLICVKS
imidazoline_receptor_candidate    TSNIQEQLLPFDLSIFKSLHQVEISHCDAKHIRGLVASKPTLATLSVRFS
                                         .:.:  *::*:::*:      : *:     *  *    *

FL1-18_SPLICE_VARIANT             LQALEELLSACGGDFCSALP--------------WLALLSANFSYNALT
FL1-18                            LQALEELLSACGGDFCSALP--------------WLALLSANFSYNALT
Drosophila_melanogaster_CG9044    LTSVDDIITRCGGDNSNGFV--------------WNELKTADFSYNSLR
imidazoline_receptor_candidate    ATSMKEVLVPEASEFDEWEPEGTTLEGPVTAVIPTWQALTTLDLSHNSIS
                                   ::.:::    ..:  .                  *   * :  ::*:*::

FL1-18_SPLICE_VARIANT             ALDSSLRLLSALRFLNLSHNQVQDCQGFLMDLCELHHLDISYNRLHLVPR
FL1-18                            ALDSSLRLLSALRFLNLSHNQVQDCQGFLMDLCELHHLDISYNRLHLVPR
Drosophila_melanogaster_CG9044    SVDTALEFAQHLQHLNLRHNKLTSVA-AIKWLPHLKTLDLSYNCLTHLPQ
imidazoline_receptor_candidate    EIDESVKLIPKIEFLDLSHNGLLVVD-NLQHLYNLVHLDLSYNKLSSLEG
                                    :*  ::.:    :..*:* ** :      :   * .*   **:*** *  :

FL1-18_SPLICE_VARIANT             -MGPSGAALGVLILRGNELRSLHGLEQLRNLRHLDLAYNLLEGHRELSPL
FL1-18                            -MGPSGAALGVLILRGNELRSLHGLEQLRNLRHLDLAYNLLEGHRELSPL
Drosophila_melanogaster_CG9044    FHMEACKRLQLLNISNNYVEELLDVAKLDALYNLDLSDNCLLEHSQLLPL
imidazoline_receptor_candidate    -LHTKLGNIKTLNLAGNLLESLSGLHKLYSLVNLDLRDNRIEQMEEVRSI
                                    :  *  : .* :..*   .: :*   *  :*** *  :      :: .:

FL1-18_SPLICE_VARIANT             WLLAELRKLYLEGNPLWFHPEHRAATAQYLSPRARDAATGFLLDGKVLSL
FL1-18                            WLLAELRKLYLEGNPLWFHPEHRAATAQYLSPRARDAATGFLLDGKVLSL
Drosophila_melanogaster_CG9044    SALMSLIVLNLQGNPLACNPKHRQATAQYLHKNS--ATVKFVLDFEPLTK
imidazoline_receptor_candidate    GSLPCLEHVSLLNNPLSIIPDYRTKVLAQFGERA----SEVCLDDTVTTE
                                    *   *   : *  .***    *.:*    .    :    .:.:     . **    :
```

Figure 8A

```
FL1-18_SPLICE_VARIANT             TDFQTHTS------LGLSPMGPP-LPWPVGSTPETSGGPDLSDSLSSG--
FL1-18                            TDFQTHTS------LGLSPMGPP-LPWPVGSTPETSGGPDLSDSLSSG--
Drosophila_melanogaster_CG9044    AEKALTGSQKWRYISGLSHRSPRSTSMSINSSSASINTSDGSQFSSFGSQ
imidazoline_receptor_candidate    KELDTVEV------LKAIQKAKE--VKSKLSNPEKKGGED-SRLSAAPCI
                                          :            .       .  *... . * *     :

FL1-18_SPLICE_VARIANT             ------G-----VVTQPLLHKVKS-RVR---VRRASISEPS--DTD----
FL1-18                            ------G-----VVTQPLLHKVKS-RVR---VRRASISEPS--DTD----
Drosophila_melanogaster_CG9044    RSVSIRGKNYTLEDNQSMDTSQSSKRISSCKIRTVDIEESSEINTDAASV
imidazoline_receptor_candidate    R----PSSSPPTVAPASASLPQPILSNQGIMFVQEEALASSLSSTDS---
                                            .                    .     .  .* .**

FL1-18_SPLICE_VARIANT             --PEPRT--------LNPSPAG------------------WFVQQHPEL
FL1-18                            --PEPRT--------LNPSPAG------------------WFVQQHPEL
Drosophila_melanogaster_CG9044    STPNPRSE-------YEEEPDNSHLETKKKIETLRLTYGNEWLKSGNAEL
imidazoline_receptor_candidate    LTPEHQPIAQGCSDSLESIPAG----QAASDDLRDVPGAVGGASPEHAEP
                                    *: :.       : * .                          :.*

FL1-18_SPLICE_VARIANT             EL-------MSSFRERFG-------RNWLQYRSHLE---PSGNP-----L
FL1-18                            EL-------MSSFRERFG-------RNWLQYRSHLE---PSGNP-----L
Drosophila_melanogaster_CG9044    MLGIE--TPQPTERERNES-----RQLFNEYLGELSGFTEAKNDSEHHNI
imidazoline_receptor_candidate    EVQVVPGSGQIIFLPFTCIGYTATNQDFIQRLSTLIR--QAIERQLPAWI
                                    :                       : : : . *   :   : :    :

FL1-18_SPLICE_VARIANT             PATPT-------TSAPSAPPASSQGPDTAPRP-----SPPQE---EARG-
FL1-18                            PATPT-------TSAPSAPPASSQGPDTAPRP-----SPPQE---EARG-
Drosophila_melanogaster_CG9044    SSTPTNNVLLASTFDATITPIKSEANDTSGQTLYETCTEGEETNYESFGN
imidazoline_receptor_candidate    EAANQRE-EGQGEQGEEEDEEEEEEDVAENRYFEMGPPDVE---EEGG
                                    ::             ..: *.: .     .    *    *  *

FL1-18_SPLICE_VARIANT             ------PQESPQ-KMSEEVRAEP----QEEE----------------E
FL1-18                            ------PQESPQ-KMSEEVRAEP----QEEE----------------E
Drosophila_melanogaster_CG9044    NTTELSTEERPPDRHEELLRLYASSSNAQDED---------------P
imidazoline_receptor_candidate    GQGE-EEEEEEEDEEAEEERLALEWALGADEDFLLEHIRILKVLWCFLIH
                                    :*    . * *          :*:

FL1-18_SPLICE_VARIANT             KEGKEEKEEGEMV--EQGEEEAGEEEEEEQ-DQKEVEAEL----CRP---
FL1-18                            KEGKEEKEEGEMV--EQGEEEAGEEEEEEQ-DQKEVEAEL----CRP---
Drosophila_melanogaster_CG9044    VSDAESDEETYIVYHEQKPSEVLFLTISSN-FIREKDTLT----ERT---
imidazoline_receptor_candidate    VQGSIRQFAACLVLTDFGIAVFEIPHQESRGSSQHILSSLRFVFCFPHGD
                                    ..  .    :*  :            ... :. :       .

FL1-18_SPLICE_VARIANT             LLVCPLEGPEG-----VRGRECFLRVTSA----HLFEVEL------QAAR
FL1-18                            LLVCPLEGPEG-----IRGRECFLRVTSA----HLFEVEL------QAAR
Drosophila_melanogaster_CG9044    KAKWSLKILESC----ERVRSNTLRINFD----TMRKDKQ------ERIY
imidazoline_receptor_candidate    LTEFGFLMPELCLVLKVRHSENTLFIISDAANLHEFHADLRSCFAPQHMA
                                    :    *        *   . * :         . .         :

FL1-18_SPLICE_VARIANT             TLERLELQSLEAAEIEPEAQAQRSPRPTGS------DLLPGAPIL-----
FL1-18                            TLERLELQSLEAAEIEPEAQAQRSPRPTGS------DLLPGAPIL-----
Drosophila_melanogaster_CG9044    CVENTLCQELEKKLRDILSQRDLTEMNISIYRCV--NCLTQFTIEQK---
imidazoline_receptor_candidate    MLCSPILYGSHTSLQEFLRQLLTFYKVAGGCQERSQGCFPVYLVYSDKRM
                                    :      .   :   *        .  . :.   .
```

Figure 8B

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```
FL1-18_SPLICE_VARIANT            ----SLRFS-----YICPDRQ------------LRR----YLVLEP-DA
FL1-18                           ----SLRFS-----YICPDRQ------------LRR----YLVLEP-DA
Drosophila_melanogaster_CG9044   ----SKRYKA--KELRCPDCRSVYVAEVTELSSSLSKPS-GEVAAEPKLS
imidazoline_receptor_candidate   VQTAAGDYSGNIEWASCTLCSAVRRSCCAPSEAVKSAAIPYWLLLTPQHL
                                     .: :.       *.                     :    *

FL1-18_SPLICE_VARIANT            HAAVQELLAVLTPVTNVAREQ-------LGEARDLLLGRFQC-------L
FL1-18                           HAAVQELLAVLTPVTNVAREQ-------LGEARDLLLGRFQC-------L
Drosophila_melanogaster_CG9044   PAMIVEESPVEELAAAINKEES----NSIGKSLASFLFYFDESSFDSNQS
imidazoline_receptor_candidate   NVIKADFNPMPNRGTHNCRNRNSFKLSRVPLSTVLLDPTRSCTQ-PRGAF
                                     .      :  .:    :     ::.       :  :     :  .

FL1-18_SPLICE_VARIANT            RCG--------HEFKPEEPRMGLDSE------EGWRP-LFQKTESPAVCP
FL1-18                           RCG--------HEFKPEEPRMGLDSE------EGWRP-LFQKTGS-----
Drosophila_melanogaster_CG9044   VVGSSNTDRD-MEFRANESDVDIISNPSQSSIEVLDPNYVQSASRKTSEE
imidazoline_receptor_candidate   ADGHVLELLVGYRFVTAIFVLPHEKFHFLRVYNQLRA-SLQDLKTVVIAK
                                     *          .* .     :       :      :     .*.

FL1-18_SPLICE_VARIANT            NCGSDHVVLLAVSRGTPNRERKQGEQSLAPSPFASPVCHPPGHGDHLDRA
FL1-18                           --GNRESSLWLLLR-LP--------ALSATLLAMVTTLTGPRTAHL-RH
Drosophila_melanogaster_CG9044   RRISQLPHLETIHDEVAK-SKSFIEREFGQLLAEQAQPTTPSTAAPLAPA
imidazoline_receptor_candidate   TPGTGGSPQGSFADGQPAERRASNDQRPQEVPAEALAPAPVEVPAPAPAA
                                              .       :  :.

FL1-18_SPLICE_VARIANT            KNSP-P-QAPSTRDHGSW-----------SLSPPPERCGLRSVDHRLRL
FL1-18                           R-------APVTMVVG--------------ASVPP--------------
Drosophila_melanogaster_CG9044   KSAV-PSHVPLTESSSSGSVTDSICTTYEQQATDAPQNLQNSLLTESSNS
imidazoline_receptor_candidate   ASASGPAKTPAPAEASTSALVP--EETPVEAPAPPPAEAPAQYPSEHLIQ
                                     .      ..*  .      .    :  . .*  .

FL1-18_SPLICE_VARIANT            FLDVEV-----FSDAQEEFQCCLKVPVALAGHTGEFMCLVVVSDRRLYLL
FL1-18                           -----------------------LSAVAS-------ALWTTDS-----
Drosophila_melanogaster_CG9044   QVSGSD-----AESNSRLKSAEDASLLPFASVFQSTNLLMSSSKKLIESE
imidazoline_receptor_candidate   ATSEENQIPSHLPACPSLRHVASLRGSAIIELFHSSIAEVENEELRHLMW
                                              ..        .         :    .

FL1-18_SPLICE_VARIANT            KVTGEMREPPASWLQLTLAVPLQDLSGIELGL---AGQSLRLEWAAGAG-
FL1-18                           ---------GSSWMLRCSAMPRRSSS---------AASRCQWHWQATLGS
Drosophila_melanogaster_CG9044   ATVFGTQPYKFNYSDFNDIDHRLKLYFYQRKF---KEDGEHFKWLAKGRI
imidazoline_receptor_candidate   SSVVFYQTPGLEVTACVLLSTKAVYFVLHDGLRRYFSEPLQDFWHQKNTD
                                           .       .           .     .  : *

FL1-18_SPLICE_VARIANT            -------RCVLLPRDARHCRAFLEELLDVLQSLPPAWRNCVS--ATEEEV
FL1-18                           -------SCALWLCLTAGCTC----------------------------
Drosophila_melanogaster_CG9044   YN-EQTQSLGEGLVVMSNCKCYLMEAFAEPHDDVAKWLRQVVSVAVNRLV
imidazoline_receptor_candidate   YNNSPFHISQCFVLKLSDLQSVNVGLFDQHFRLTGSTPMQVVTCLTRDSY
                                              .

FL1-18_SPLICE_VARIANT            TPQHRLWPLLEKDSSLEARQFFYLR----------AFLVEGPSTCLVS--
FL1-18                           --------------------------------------------------
Drosophila_melanogaster_CG9044   AIDLLPWKLGLSFTLKDWGGFVLLLHDMLRTESLLNYLQQIPLPEQCK--
imidazoline_receptor_candidate   LTHCFLQHLMVVLSSLERTPSPEPVDKDFYSEFGNKTTGKMENYELIHSS
                                           .         :                      :
```

Figure 8C

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     FL1-18_SPLICE_VARIANT              --LLLTPS------TLFLLDEDAAGSP----------------AEPS---
     FL1-18                            --------------------------------------------------------
     Drosophila_melanogaster_CG9044    --LNHQPS------VTLSHQWETIASEPVKMCSLIPSCQWICDQEKSS--
5    imidazoline_receptor_candidate    RVKFTYPSEEEIGDLTFTVAQKMAEPEKAPALSILLYVQAFQVGMPPPGC
                                                    .                  .             .

     FL1-18_SPLICE_VARIANT             -----PPAASGEASEKVPPSGPG----PAVRVREQ---QPLSSLSS----
     FL1-18                            --------------------------------------------------------
10   Drosophila_melanogaster_CG9044    ----FEPSLLLITETHLYISGNGKFSWLSDKVQEKP-IQPELSLNQP---
     imidazoline_receptor_candidate    CRGPLRPKTLLLTSSEIFLLDEDCVHYPLPEFAKEPPQRDRYRLDDGRRV
                                                    .  .         . ::        .    ..

     FL1-18_SPLICE_VARIANT             ------VLLYRSAPEDLRLLFYD----------------EV--------S
     FL1-18                            --------------------------------------------------------
15   Drosophila_melanogaster_CG9044    --LSNLVDVERITDQKYAINFID----------------ET--------Q
     imidazoline_receptor_candidate    RDLDRVLMGYQTYPQALTLVFDDVQGHDLMGSVTLDHFGEVPGGPARASQ
                                                .   :          :                 :          .

     FL1-18_SPLICE_VARIANT             RLESFWALRVVCQEQLTALLAWIREPWEELFSIGLRTVIQEALALDR
     FL1-18                            -----------------------------------------------
20   Drosophila_melanogaster_CG9044    NRCEIWKLQFETHANAACCLNVIGKGWEQLFGVPFSLSGT-------
     imidazoline_receptor_candidate    GREVQWQVFVPSAESREKLISLLARQWEALCGRELPVELTG------
                                                .   .  :              :.
```

(* REPRESENTS RESIDUES THAT ARE IDENTICAL IN ALL FOUR PRTEINS; : REPRESENTS RESIDUES THAT ARE OF SIMILAR BIOCHEMICAL CHARACTER IN 3 OUT OF THE 4 PROTEINS; . REPRESENTS RESIDUES THAT ARE OF SIMILAR BIOCHEMICAL CAHARACTER IN 2 OUT OF THE 4 PROTEINS).
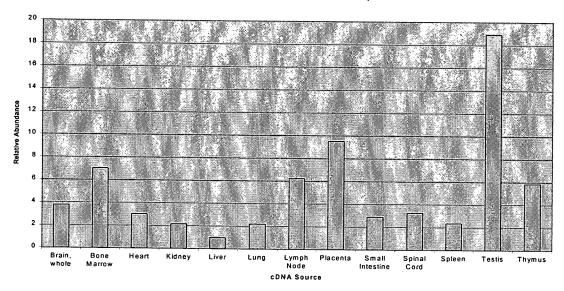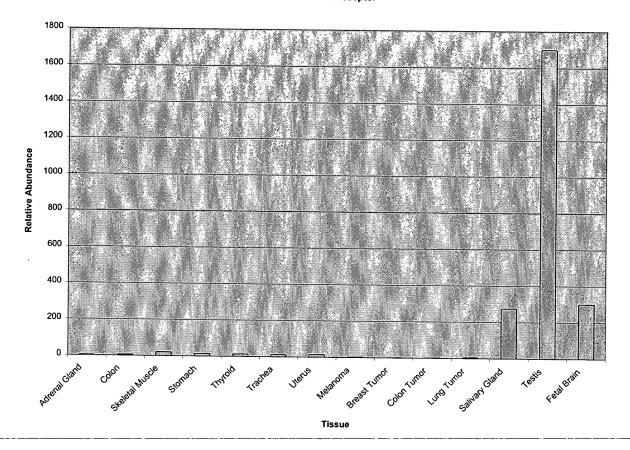
Figure 8D

Incyte-2499870 Imidazoline-related Receptor

Figure 9.

FL1 - Imidazoline Receptor

Figure 10.